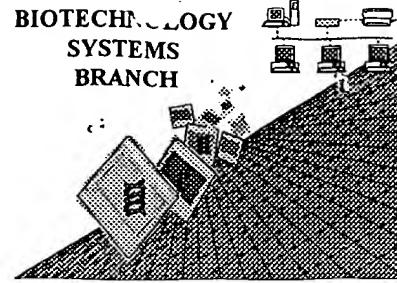


Hair

BEST AVAILABLE COPY
RAW SEQUENCE LISTING
ERROR REPORT



FH

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/474,980A
Source: 1647
Date Processed by STIC: 3/22/2001

RECEIVED

APR 02 2001

TECH CENTER 1600/2900

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:
<http://www.uspto.gov/web/offices/pac/checker>

Raw Sequence Listing Error Summary

ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER: 09/474,980A

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- | | | |
|----|---------------------------------------|---|
| 1 | ____ Wrapped Nucleic | The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping". |
| 2 | ____ Wrapped Aminos | The amino acid number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping". |
| 3 | ____ Incorrect Line Length | The rules require that a line not exceed 72 characters in length. This includes spaces. |
| 4 | ____ Misaligned Amino Acid Numbering | The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers. |
| 5 | ____ Non-ASCII | This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed. |
| 6 | ____ Variable Length | Sequence(s) ____ contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and indicate in the (ix) feature section that some may be missing. |
| 7 | ____ PatentIn ver. 2.0 "bug" | A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies primarily to the mandatory <220>-<223> sections for Artificial or Unknown sequences. |
| 8 | ____ Skipped Sequences (OLD RULES) | Sequence(s) ____ missing. If intentional, please use the following format for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X:
(i) SEQUENCE CHARACTERISTICS: (Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s). |
| 9 | ____ Skipped Sequences (NEW RULES) | Sequence(s) ____ missing. If intentional, please use the following format for each skipped sequence.
<210> sequence id number
<400> sequence id number
000 |
| 10 | ____ Use of n's or Xaa's (NEW RULES) | Use of n's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents. |
| 11 | ____ Use of <213>Organism (NEW RULES) | Sequence(s) ____ are missing this mandatory field or its response. |
| 12 | ____ Use of <220>Feature (NEW RULES) | Sequence(s) ____ are missing the <220>Feature and associated headings.
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules) |
| 13 | ____ PatentIn ver. 2.0 "bug" | Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other means to copy file to floppy disk. |

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/474,980A

DATE: 03/22/2001
TIME: 16:17:41

Input Set : A:\60292668.txt
Output Set: N:\CRF3\03222001\I474980A.raw

Does Not Comply
Corrected Diskette Needed

3 <110> APPLICANT: JOHNSON Jr., Eugene M.
4 MILBRANDT, Jeffrey D.
5 KOTZBAUER, Paul T.
6 LAMPE, Patricia A.
7 KLEIN, Robert
8 DESAUVAGE, Fred
10 <120> TITLE OF INVENTION: Persephin and Related Growth Factors
12 <130> FILE REFERENCE: 6029-2668
14 <140> CURRENT APPLICATION NUMBER: 09/474,980A
15 <141> CURRENT FILING DATE: 1999-12-29
17 <150> PRIOR APPLICATION NUMBER: 08/519,777
18 <151> PRIOR FILING DATE: 1995-08-28
20 <160> NUMBER OF SEQ ID NOS: 242
22 <170> SOFTWARE: Microsoft Word 97

ERRORED SEQUENCES

276 <210> SEQ ID NO: 11 594 shown
 277 <211> LENGTH: 591
 278 <212> TYPE: DNA
 279 <213> ORGANISM: Homo sapiens
 281 <400> SEQUENCE: 11
 282 atgcagcgct ggaaggcggc ggccttggcc tcagtgtct gcagctccgt gctgtccatc 60
 284 tggatgtgtc gagaggcgct gcttctcagc caccgctcg gacctgcgt ggtccccctg 120
 286 caccgcctgc ctgcgaaccct ggacgcccgg attgcccggc tggcccaagta ccgtgcactc 180
 288 ctgcaggggg ccccgatgc gatggagctg cgccgatgc cgccctggc tggccggccc 240
 290 ccagggtccgc gccgtggcggc gggggcccccgg cgccggcgcc cgccgtgcgcg gttgggggcg 300
 292 cggccttgctc ggctgcgcga gctggagggtg cgccgtgcgcg agctgggcct ggctacgcg 360
 294 tccgacgaga cggtgtgttt ccgcgtactgc gcaggcgctc gcgaggctgc cgccgcgc 420
 296 tacgacccctcg ggctgcgcg actgcgcagg cgccggcgcc tgcggggaa ggggtgcgc 480
 298 ggcgcgcct gctgcgcggc gacgcgcctac gaggacgagg tgccttcct ggacgcgcac 540
 E--> 300 agccgcgtacc acacgggtcga cgagctgtcg gcgcgcgagt gcgcctgcgt gtga 594
 303 <210> SEQ ID NO: 12
 304 <211> LENGTH: 585 588(next page)
 305 <212> TYPE: DNA
 306 <213> ORGANISM: Mus musculus
 308 <400> SEQUENCE: 12
 309 atgaggcgct ggaaggcagg ggccttggtg tcgtctcatct gcagctccct gctatctgtc 60
 311 tggatgtgcc aggagggtct gctttgggc caccgctgg gacccgcgt tgccccgcta 120
 313 cgacgccttc cacgcacccct ggacgcccgc atgcgcgc tggcccaagta tcgcgtctg 180
 315 ctccaggcgcc ccccccacgc ggtggagctt cgagaactttt ctccctggc tgccccgcac 240
 317 ccgggacccgc gccgtgcgcg ggttccccgg cgccggcgcc cgccggccggg ggctcgccct 300
 319 tgtgggtcgc gcgagctcga ggtgcgcgtg agcgagctgg gcctgggcta cacgtcgat 360
 321 gagaccgtgc tggccgcata ctgcgcaggc gcgtgcgagg cggccatccg catctacgac 420
 323 ctgggccttc ggccgcgtcg ccagcggagg cgccgtgcgcgca gagagcgggc gggggcgcac 480
 325 cggtgttgc gccccacggc ctatgaggac gaggtgtctt tcctggacgt gacacagccgc 540

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/474,980A

DATE: 03/22/2001
TIME: 16:17:41

Input Set : A:\60292668.txt
Output Set: N:\CRF3\03222001\I474980A.raw

E--> 327 taccacacgc tgcaagagct gtcggcgcgg gagtgcgctg gcgtgtga 588
 4310 <210> SEQ ID NO: 177
 4311 <211> LENGTH: 723
 4312 <212> TYPE: DNA
 4313 <213> ORGANISM: Mus musculus
 E--> 4315 <400> SEQUENCE: (153) 177<
 4316 atggctgcag gaaggacttgcg gatccctgtgt ctgtgtgcctc tgtcctgtca cccgagcctc 60
 4318 ggctgggtcc ttgatcttca agaggcttct gtggcagata agctcttcatt tggttaagatg 120
 4320 gcagagactc gggggacttgc gacggcccat cagggttaaga attccctgggg gcctcccgac 180
 4322 tcccccaattc cttcttcaa agcgcctcatc ttgccttaca atcctactct accttgcact 240
 4324 aggttacaacac catgtccgtc ttccaagacg cttggcttgt tcatgccgac tggggaccc 300
 4326 gaccctacca gtggctgagc tgggcctggg ctatgcctcg gaggagaagg tcatcttccg 360
 4328 atactgtgtc ggcaactgtc cccaaaggagc ccgttaccccg cacagtctgg tactggcccg 420
 4330 gtttgggggg cggggctgag cccatggccg accctgttcg cagccccacca gctatgtcga 480
 4332 tttttttttt cttgtatgtc acggccatgg gcacggctgtc cttcgtctc cagctgcac 540
 4334 ttgtggctgt ggtggctgaa ggaggccagt ctgggtgtctc agaatcacaa gcatgagaca 600
 4336 ggctgggctt taaaaggctc aggtgacatt actagaaatt tgcataaggta aagataagaa 660
 4338 gggaaaggac cagggtttt ttgtttttt ctttgcattt ttgttagttt tttttttttt 720
 4340 ttt 723
 4396 <210> SEQ ID NO: 180
 4397 <211> LENGTH: (106) 471
 4398 <212> TYPE: DNA
 4399 <213> ORGANISM: Mus musculus
 4401 <400> SEQUENCE: 180
 4402 tcagccacca cagccacaaag ctgcagctga gagctgaggc agctgtgcc aatgggtgtg 60
 4404 atcatcaagg aaggctcacat cagcatagct ggtggctgg cagcagggtc ggccatggc 120
 4406 tcgaccggc cctcgaaagcc gggccagttac cagactgtgc tgggtacggg cctttgggg 180
 4408 acagctgcca gcacagtata ggaatgtac ttcttcctcc gaggcatagc ccaggcccac 240
 4410 ctcagccactt ggttaggtca ggctccacag tggcatgaa ccagccaaagg ctcttggaaag 300
 4412 acggacatgg ttgttaccctt gatggggcgtt ccaggccctt ctatctctg ccatcttccc 360
 4414 aaatggatggc ttatctgcca cagaaggctt tcggatgtca aggaccaggc cgaggctcg 420
 E--> 4416 gtgcaaggac aggaggcagca gacacaggat ccaaggctt cctgcagcca t 471
 5114 <210> SEQ ID NO: 219
 5115 <211> LENGTH: (180) 23
 5116 <212> TYPE: PRT
 5117 <213> ORGANISM: Homo sapiens
 5119 <400> SEQUENCE: 219
 5120 Met Ala Val Gly Lys Phe Leu Leu Gly Ser Leu Leu Leu Leu Ser Leu
 5121 1 5 10 15
 5123 Gln Leu Gly Gln Gly Trp Gly
 E--> 5124 20
 5576 <210> SEQ ID NO: 242
 5577 <211> LENGTH: 93
 5578 <212> TYPE: PRT
 5579 <213> ORGANISM: Mus musculus *next page*
 5581 <400> SEQUENCE: 242
 5582 Cys Val Leu Thr Ala Ile His Leu Asn Val Thr Asp Leu Gly Leu Gly
 5583 5 10 15
 5585 Tyr Glu Thr Lys Glu Glu Leu Ile Phe Arg Tyr Cys Ser Gly Ser Cys

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/474,980A

DATE: 03/22/2001
TIME: 16:17:42

Input Set : A:\60292668.txt
Output Set: N:\CRF3\03222001\I474980A.raw

5586 20 25 30
5588 Glu Ser Ala Glu Thr Met Tyr Asp Lys Ile Leu Lys Asn Leu Ser Arg
5589 35 40 45
5591 Ser Arg Arg Leu Thr Ser Asp Lys Val Gly Gln Ala Cys Cys Arg Pro
5592 50 55 60
5594 Val Ala Phe Asp Asp Asp Leu Ser Phe Leu Asp Asp Asn Leu Val Tyr
5595 65 70 75 80
5597 His Ile Leu Arg Lys His Ser Ala Lys Arg Cys Gly Cys
5598 85 90

E--> 5601 151

E--> 5602 24699.doc

delete

see next page for more errors

09/4/98 4,980A 4

<210> 45
<211> 29
<212> DNA
<213> Homo sapiens

<400> 45
tcrtantcrw angonryngg nckrcarca

see item 10 on Error Summary Sheet

29

FYI:

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

VERIFICATION SUMMARY DATE: 03/22/2001
PATENT APPLICATION: US/09/474,980A TIME: 16:17:43

Input Set : A:\60292668.txt
Output Set: N:\CRF3\03222001\I474980A.raw

L:86 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:3
L:91 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:101 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:4
L:106 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:4
L:111 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:121 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:5
L:126 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:5
L:131 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:134 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:300 M:252 E: No. of Seq. differs, <211> LENGTH: Input:591 Found:594 SEQ:11
L:327 M:252 E: No. of Seq. differs, <211> LENGTH: Input:585 Found:588 SEQ:12
L:688 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:33
L:693 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:33
L:698 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:33
L:708 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:34
L:713 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:34
L:718 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:34
L:723 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:34
L:728 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:34
L:733 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:34
L:738 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:34
L:743 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:34
L:753 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:35
L:758 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:35
L:763 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:35
L:768 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:35
L:773 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:35
L:778 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:35
L:788 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:36
L:793 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:36
L:798 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:36
L:803 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:36
L:808 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:36
L:818 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:37
L:823 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:37
L:828 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:37
L:833 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:37
L:838 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:37
L:848 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:38
L:853 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:38
L:858 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:38
L:863 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:38
L:868 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:38
L:878 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:39
L:883 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:39
L:888 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:39
L:893 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:39
L:898 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:39

VERIFICATION SUMMARY
PATENT APPLICATION: US/09/474,980A

DATE: 03/22/2001
TIME: 16:17:43

Input Set : A:\60292668.txt
Output Set: N:\CRF3\03222001\I474980A.raw

L:908 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:40
L:913 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:40
L:918 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:40
L:923 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:40
L:933 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:41
L:938 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:41
L:943 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:41
L:948 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:41
L:953 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:41
L:958 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:41
L:963 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:41
L:1028 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:42
L:1117 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:43
L:1206 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:44
L:1215 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:45
L:1215 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:45
L:1215 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:45
L:1215 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:45
L:1215 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:45
L:1294 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:46
L:1358 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:47
L:1472 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:48
L:1531 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:50
L:1537 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (51) SEQUENCE:
L:1570 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:52
L:2356 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (104) SEQUENCE:
L:2442 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:108
L:2462 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:109
L:2492 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:110
L:2571 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:113
L:2626 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:114
L:2671 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:115
L:2724 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:116
L:2782 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:117
L:2850 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:118
L:2898 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:119
L:2946 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:120
L:3004 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:121
L:3062 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:122
L:3130 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:123
L:3203 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:124
L:3221 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:125
L:3256 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:126
L:3276 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:127
L:3296 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:128
L:3316 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:129
L:3341 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:130
L:3408 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (133) SEQUENCE:
L:3525 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:142

VERIFICATION SUMMARY DATE: 03/22/2001
PATENT APPLICATION: US/09/474,980A **TIME:** 16:17:43

Input Set : A:\60292668.txt
Output Set: N:\CRF3\03222001\I474980A.raw

L:3554 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:145
L:4315 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:177 differs:153
L:4416 M:252 E: No. of Seq. differs, <211>LENGTH:Input:106 Found:471 SEQ:180
L:4922 M:283 W: Missing Blank Line separator, <400> field identifier
L:5124 M:252 E: No. of Seq. differs, <211>LENGTH:Input:180 Found:23 SEQ:219
L:5601 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:242
L:5602 M:333 E: Wrong sequence grouping, Amino acids not in groups!